

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/577,601  
Source: IFWP  
Date Processed by STIC: 05/11/2006

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 05/11/2006

PATENT APPLICATION: US/10/577,601

TIME: 11:12:42

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\05112006\J577601.raw

3 &lt;110&gt; APPLICANT: KANEKA CORPORATION

5 &lt;120&gt; TITLE OF INVENTION: NOVEL ACETOACETYL-CoA REDUCTASE AND PROCESS FOR PRODUCING OPTICALLY

6 ACTIVE ALCOHOL

8 &lt;130&gt; FILE REFERENCE: BO30435WO01

C--&gt; 10 &lt;140&gt; CURRENT APPLICATION NUMBER: US/10/577,601

C--&gt; 10 &lt;141&gt; CURRENT FILING DATE: 2006-04-27

10 &lt;150&gt; PRIOR APPLICATION NUMBER: JP2003-380987

11 &lt;151&gt; PRIOR FILING DATE: 2003-11-11

13 &lt;160&gt; NUMBER OF SEQ ID NOS: 15

15 &lt;170&gt; SOFTWARE: PatentIn version 3.1

17 &lt;210&gt; SEQ ID NO: 1

18 &lt;211&gt; LENGTH: 245

19 &lt;212&gt; TYPE: PRT

20 <213> ORGANISM: *Achromobacter xylosoxidans* subsp. *denitrificans*

22 &lt;400&gt; SEQUENCE: 1

23 Met Ser Gly Lys Leu Ala Tyr Val Thr Gly Gly Met Gly Gly Ile Gly

24 1 5 10 15

26 Thr Ser Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg Val Val Ala

27 20 25 30

29 Gly Cys Gly Pro Ser Arg Asn Tyr Gln Gln Trp Leu Asp Glu Gln Ala

30 35 40 45

32 Ala Gln Gly Tyr Thr Phe Tyr Ala Ser Val Gly Asn Val Ser Asp Trp

33 50 55 60

35 Glu Ser Thr Val Glu Ala Phe Glu Arg Val Lys Arg Asp Met Gly Pro

36 65 70 75 80

38 Val Asp Val Leu Val Asn Asn Ala Gly Ile Thr Arg Asp Gly Leu Phe

39 85 90 95

41 Arg Lys Met Ser Ala Asp Asp Trp Arg Ala Val Ile Asp Thr Asn Leu

42 100 105 110

44 Asn Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp Asp Met Val Glu

45 115 120 125

47 Arg Gln Trp Gly Arg Ile Val Asn Ile Ser Ser Val Asn Gly Gln Lys

48 130 135 140

50 Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys Ala Gly Ile His

51 145 150 155 160

53 Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Ser Lys Gly Ile Thr

54 165 170 175

56 Val Asn Thr Val Ser Pro Gly Tyr Ile Gly Thr Asp Met Val Arg Ala

57 180 185 190

59 Ile Arg Pro Asp Val Leu Glu Lys Ile Val Ala Thr Ile Pro Val Arg

60 195 200 205

62 Arg Leu Gly Thr Pro Glu Glu Ile Ala Ser Ile Thr Ser Trp Leu Ala

63 210 215 220

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```

65 Ser Asp Glu Ser Gly Phe Ser Thr Gly Ala Asp Phe Ser Leu Asn Gly
66 225                230                235                240
68 Gly Leu His Met Gly
69                245
72 <210> SEQ ID NO: 2
73 <211> LENGTH: 738
74 <212> TYPE: DNA
75 <213> ORGANISM: Achromobacter xylosoxidans subsp. denitrificans
77 <220> FEATURE:
78 <221> NAME/KEY: CDS
79 <222> LOCATION: (1)..(738)
81 <400> SEQUENCE: 2
82 atg agc gga aaa ctg gct tac gtt aca ggc ggg atg ggc ggt atc ggc      48
83 Met Ser Gly Lys Leu Ala Tyr Val Thr Gly Gly Met Gly Gly Ile Gly
84 1                5                10                15
86 acc tca att tgc cag cgc ctg gcc aaa gat ggc ttt cgc gtg gtg gca      96
87 Thr Ser Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg Val Val Ala
88                20                25                30
90 ggc tgc ggc ccc agc cgc aat tac cag caa tgg ctg gat gaa cag gcg      144
91 Gly Cys Gly Pro Ser Arg Asn Tyr Gln Gln Trp Leu Asp Glu Gln Ala
92                35                40                45
94 gcg cag ggc tat acg ttc tac gcg tca gtg ggc aac gtg tcc gat tgg      192
95 Ala Gln Gly Tyr Thr Phe Tyr Ala Ser Val Gly Asn Val Ser Asp Trp
96                50                55                60
98 gag tcc acg gta gaa gca ttc gag cgc gtc aag cgg gac atg ggc ccg      240
99 Glu Ser Thr Val Glu Ala Phe Glu Arg Val Lys Arg Asp Met Gly Pro
100 65                70                75                80
102 gtc gat gtg ctg gtc aac aac gcg ggc atc acc cgc gac ggc ctg ttc      288
103 Val Asp Val Leu Val Asn Asn Ala Gly Ile Thr Arg Asp Gly Leu Phe
104                85                90                95
106 cgc aag atg agc gcc gac gac tgg cgc gcg gtc atc gac acc aac ctg      336
107 Arg Lys Met Ser Ala Asp Asp Trp Arg Ala Val Ile Asp Thr Asn Leu
108                100                105                110
110 aac agc ctc ttc aac gtg acc aag cag gtg atc gac gac atg gtc gag      384
111 Asn Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp Asp Met Val Glu
112                115                120                125
114 cgc cag tgg ggc cgc atc gtc aac atc agc tcg gtg aac ggg cag aag      432
115 Arg Gln Trp Gly Arg Ile Val Asn Ile Ser Ser Val Asn Gly Gln Lys
116                130                135                140
118 ggg cag ttc ggc cag acg aac tat tcc acg gcg aag gcg ggc atc cat      480
119 Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys Ala Gly Ile His
120 145                150                155                160
122 ggc ttc acc atg gcg ctg gcg cag gaa gtg gcc agc aag ggc atc acg      528
123 Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Ser Lys Gly Ile Thr
124                165                170                175
126 gtc aac acg gtg tcg ccg ggc tac atc ggc acg gac atg gtt cgc gcc      576
127 Val Asn Thr Val Ser Pro Gly Tyr Ile Gly Thr Asp Met Val Arg Ala
128                180                185                190
130 atc cgt ccg gac gtg ctg gaa aag atc gtc gcc acc att ccg gtg cgc      624

```

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Input Set : A:\PTO.RJ.txt

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```

131 Ile Arg Pro Asp Val Leu Glu Lys Ile Val Ala Thr Ile Pro Val Arg
132      195      200      205
134 cgc ctg ggc acg ccg gag gaa atc gcg tcc atc acg tcg tgg ctg gcc      672
135 Arg Leu Gly Thr Pro Glu Glu Ile Ala Ser Ile Thr Ser Trp Leu Ala
136      210      215      220
138 tcg gat gag tct ggg ttt tcg acg ggc gcg gac ttc tcg ctc aac ggc      720
139 Ser Asp Glu Ser Gly Phe Ser Thr Gly Ala Asp Phe Ser Leu Asn Gly
140 225      230      235      240
142 ggc ctg cat atg ggc tga      738
143 Gly Leu His Met Gly
144      245
147 <210> SEQ ID NO: 3
148 <211> LENGTH: 246
149 <212> TYPE: PRT
150 <213> ORGANISM: Ralstonia eutropha
152 <400> SEQUENCE: 3
153 Met Thr Gln Arg Ile Ala Tyr Val Thr Gly Gly Met Gly Gly Ile Gly
154 1      5      10      15
156 Thr Ala Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg Val Val Ala
157      20      25      30
159 Gly Cys Gly Pro Asn Ser Pro Arg Glu Lys Trp Leu Glu Gln Gln
160      35      40      45
162 Lys Ala Leu Gly Phe Asp Phe Ile Ala Ser Glu Gly Asn Val Ala Asp
163      50      55      60
165 Trp Asp Ser Thr Lys Thr Ala Phe Asp Lys Val Lys Ser Glu Val Gly
166 65      70      75      80
168 Glu Val Asp Val Leu Ile Asn Asn Ala Gly Ile Thr Arg Asp Val Val
169      85      90      95
171 Phe Arg Lys Met Thr Arg Ala Asp Trp Asp Ala Val Ile Asp Thr Asn
172      100      105      110
174 Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp Gly Met Ala
175      115      120      125
177 Asp Arg Gly Trp Gly Arg Ile Val Asn Ile Ser Ser Val Asn Gly Gln
178      130      135      140
180 Lys Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys Ala Gly Leu
181 145      150      155      160
183 His Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Thr Lys Gly Val
184      165      170      175
186 Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Ala Thr Asp Met Val Lys
187      180      185      190
189 Ala Ile Arg Gln Asp Val Leu Asp Lys Ile Val Ala Thr Ile Pro Val
190      195      200      205
192 Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys Ala Trp Leu
193      210      215      220
195 Ser Ser Glu Glu Ser Gly Phe Ser Thr Gly Ala Asp Phe Ser Leu Asn
196 225      230      235      240
198 Gly Gly Leu His Met Gly
199      245
202 <210> SEQ ID NO: 4

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## RAW SEQUENCE LISTING

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TIME: 11:12:42

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\05112006\J577601.raw

```

203 <211> LENGTH: 741
204 <212> TYPE: DNA
205 <213> ORGANISM: Ralstonia eutropha
207 <220> FEATURE:
208 <221> NAME/KEY: CDS
209 <222> LOCATION: (1)..(741)
211 <400> SEQUENCE: 4
212 atg act cag cgc att gcg tat gtg acc ggc ggc atg ggt ggt atc gga      48
213 Met Thr Gln Arg Ile Ala Tyr Val Thr Gly Gly Met Gly Gly Ile Gly
214 1          5          10          15
216 acc gcc att tgc cag cgg ctg gcc aag gat ggc ttt cgt gtg gtg gcc      96
217 Thr Ala Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg Val Val Ala
218          20          25          30
220 ggt tgc ggc ccc aac tcg ccg cgc cgc gaa aag tgg ctg gag cag cag      144
221 Gly Cys Gly Pro Asn Ser Pro Arg Arg Glu Lys Trp Leu Glu Gln Gln
222          35          40          45
224 aag gcc ctg ggc ttc gat ttc att gcc tcg gaa ggc aat gtg gct gac      192
225 Lys Ala Leu Gly Phe Asp Phe Ile Ala Ser Glu Gly Asn Val Ala Asp
226          50          55          60
228 tgg gac tcg acc aag acc gca ttc gac aag gtc aag tcc gag gtc ggc      240
229 Trp Asp Ser Thr Lys Thr Ala Phe Asp Lys Val Lys Ser Glu Val Gly
230 65          70          75          80
232 gag gtt gat gtg ctg atc aac aac gcc ggt atc acc cgc gac gtg gtg      288
233 Glu Val Asp Val Leu Ile Asn Asn Ala Gly Ile Thr Arg Asp Val Val
234          85          90          95
236 ttc cgc aag atg acc cgc gcc gac tgg gat gcg gtg atc gac acc aac      336
237 Phe Arg Lys Met Thr Arg Ala Asp Trp Asp Ala Val Ile Asp Thr Asn
238          100          105          110
240 ctg acc tcg ctg ttc aac gtc acc aag cag gtg atc gac ggc atg gcc      384
241 Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp Gly Met Ala
242          115          120          125
244 gac cgt ggc tgg ggc cgc atc gtc aac atc tcg tcg gtg aac ggg cag      432
245 Asp Arg Gly Trp Gly Arg Ile Val Asn Ile Ser Ser Val Asn Gly Gln
246          130          135          140
248 aag ggc cag ttc ggc cag acc aac tac tcc acc gcc aag gcc ggc ctg      480
249 Lys Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys Ala Gly Leu
250 145          150          155          160
252 cat ggc ttc acc atg gca ctg gcg cag gaa gtg gcg acc aag ggc gtg      528
253 His Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Thr Lys Gly Val
254          165          170          175
256 acc gtc aac acg gtc tct ccg ggc tat atc gcc acc gac atg gtc aag      576
257 Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Ala Thr Asp Met Val Lys
258          180          185          190
260 gcg atc cgc cag gac gtg ctc gac aag atc gtc gcg acg atc ccg gtc      624
261 Ala Ile Arg Gln Asp Val Leu Asp Lys Ile Val Ala Thr Ile Pro Val
262          195          200          205
264 aag cgc ctg ggc ctg ccg gaa gag atc gcc tcg atc tgc gcc tgg ttg      672
265 Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys Ala Trp Leu
266          210          215          220

```

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DATE: 05/11/2006

PATENT APPLICATION: US/10/577,601

TIME: 11:12:42

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\05112006\J577601.raw

```

268 tcg tcg gag gag tcc ggt ttc tcg acc ggc gcc gac ttc tcg ctc aac      720
269 Ser Ser Glu Glu Ser Gly Phe Ser Thr Gly Ala Asp Phe Ser Leu Asn
270 225                230                235                240
272 ggc ggc ctg cat atg ggc tga      741
273 Gly Gly Leu His Met Gly
274                245
277 <210> SEQ ID NO: 5
278 <211> LENGTH: 19
279 <212> TYPE: DNA
280 <213> ORGANISM: Artificial Sequence
282 <220> FEATURE:
283 <223> OTHER INFORMATION: Primer 1
285 <220> FEATURE:
286 <221> NAME/KEY: misc_feature
287 <222> LOCATION: (6)..(6)
288 <223> OTHER INFORMATION: n represents a, t, g or c
290 <220> FEATURE:
291 <221> NAME/KEY: misc_feature
292 <222> LOCATION: (12)..(12)
293 <223> OTHER INFORMATION: n represents a, t, g or c
295 <400> SEQUENCE: 5
W--> 296 carggntaya cnttytayg      19
299 <210> SEQ ID NO: 6
300 <211> LENGTH: 20
301 <212> TYPE: DNA
302 <213> ORGANISM: Artificial Sequence
304 <220> FEATURE:
305 <223> OTHER INFORMATION: Primer 2
307 <220> FEATURE:
308 <221> NAME/KEY: misc_feature
309 <222> LOCATION: (12)..(12)
310 <223> OTHER INFORMATION: n represents a, t, g or c
312 <220> FEATURE:
313 <221> NAME/KEY: misc_feature
314 <222> LOCATION: (15)..(15)
315 <223> OTHER INFORMATION: n represents a, t, g or c
317 <400> SEQUENCE: 6
W--> 318 gcdatytcyt cnggngtycc      20
321 <210> SEQ ID NO: 7
322 <211> LENGTH: 25
323 <212> TYPE: DNA
324 <213> ORGANISM: Artificial Sequence
326 <220> FEATURE:
327 <223> OTHER INFORMATION: Primer 3
329 <400> SEQUENCE: 7
330 cgtcggcgct catcttgcgg aacag      25
333 <210> SEQ ID NO: 8
334 <211> LENGTH: 25
335 <212> TYPE: DNA

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/577,601

DATE: 05/11/2006  
TIME: 11:12:43

Input Set : A:\PTO.RJ.txt  
Output Set: N:\CRF4\05112006\J577601.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 6, 12  
Seq#:6; N Pos. 11, 15

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/577,601

DATE: 05/11/2006

TIME: 11:12:43

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\05112006\J577601.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0

L:318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0